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KIM MARSHALL
MANAGER EXAMINATION SUPPORT AND
SALES

AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis sequences

The invention is described in the following statement:

P. gingivalis sequences

FIELD OF THE INVENTION

5 The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

10 Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated
15 with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically
20 cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of
25 the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

P. gingivalis is a black-pigmented, anaerobic, asaccharolytic,
30 proteolytic Gram-negative rod that obtains energy from the metabolism of

specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown *in vitro* it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy. DNA sequences that were considered to be poor vaccine candidates and not selected include those that code for proteins involved in replication, non-essential proteins involved in cellular processes and those proteins present at sites that would be unlikely to be affected by immune mediators such as those found in the bacterial cytoplasm or inner membranes.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, fragments thereof and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, fragments thereof and sequences complementary thereto.

In a third aspect the present invention consists in an isolated *P. gingivalis* polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18 or fragments thereof.

In a fourth aspect the present invention consists in an isolated polynucleotide, the polynucleotide encoding a polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18 or fragments thereof.

In a fourth aspect the present invention consists in a nucleotide probe specific for *P. gingivalis*, the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and sequences complementary thereto.

In a fifth aspect the present invention consists in a composition for use in raising an immune response in an animal directed against *P.*

Gingivalis the composition including an acceptable carrier and/or adjuvant and at least one polypeptide having a sequence selected from the group
5 consisting of SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18 or fragments thereof.

As will be understood by those skilled in the art the nucleotides of the present invention may be useful in DNA vaccination to reduce the incidence
10 and/or severity of *P. gingivalis* infection.

Accordingly in a sixth aspect the present invention consists in a composition for use in inducing an immune response, the composition including at least one DNA molecule, the at least one DNA molecule having or including a sequence selected from the group consisting of SEQ ID NO: 1,
15 SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, fragments thereof and sequences complementary thereto.

Further information regarding DNA vaccination may be found in Donnelly *et al*, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

20 Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

25

DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961)(1). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995)(2). Briefly, purified
 5 genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and
 10 electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli
 15 Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded
 20 for the extraction of plasmid DNA for sequencing.

DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep
 25 well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready
 30 Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems,

Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM
 5 377 DNA sequencers (PE Applied Biosystems).

The sequences obtained are set out below.

SeqID#1-9 represents the DNA sequence that encodes proteins in SeqID#10-27. Proteins in SeqID#10-18 are the entire open reading frame from DNA SeqID#1-9. Proteins in SeqID#19-27 are the proteins encoded by
 10 DNA SeqID#1-9 from their putative initiation codon. The initiation codon was calculated from sequence homology alignment using FastX or by the ORF prediction program GeneMark.

As will be understood by those skilled in the art open reading frames (ORFs) may be readily identified. ORFs may be determined using two
 15 methods, for example, alignments from FastX search results may be used to define the start and end positions of coding regions if sufficient protein homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a training matrix based on published *P.gingivalis* sequences. This matrix may be further
 20 refined by adding ORFs identified from the results of homology searching and ORFs identified by GeneMark. The program PSORT (4) may be used for the detection of signal sequences and the prediction of protein cell localisation. A UNIX version of TopPred (5) may be used to identify potential membrane spanning domains.

25

DNA sequence analysis

Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed
 30 files were assembled into contigs using Staden Gap v4.1 and exported as a

consensus file in FastA format. This consensus was converted into GCG format files and analysed for homology using the FASTX algorithm on a non-redundant protein database compiled by ANGIS (Australian Genomic Information Service, University of Sydney). Individual FASTX search
5 results were examined for significant homology by statistical probability and amino acid alignments.

The results are set out in Table 1.

SeqID#	Length of protein in SeqID	Homology description	Length of protein homolog	% identity	Overlap	E value
1, 7, 13	307aa	Amylovoran outer membrane export protein, <i>Erwinia amylovora</i>	377aa	29	251aa	7.00E-06
2, 8, 14	429aa	48kD outer membrane protein, <i>Actinobacillus pleuropneumoniae</i>	449aa	32	425aa	5.70E-43
3, 9, 15	315aa	Adhesin protein, <i>Synechocystis</i> sp.	338aa	31	294aa	8.10E-14
4, 10, 16	331aa	36kD outer membrane protein, <i>Helicobacter pylori</i>	329aa	37	326aa	5.50E-43
5, 11, 17	223aa	Outer membrane porin F, <i>Pseudomonas</i> <i>fluorescens</i>	326aa	34	199aa	1.10E-11
6, 12, 18	426aa	Haeme uptake protein A, <i>Bacteroides</i> <i>fragilis</i>	431aa	80	411	9.50E- 153

Table 1

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

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ccgcaatcct ctctgatcg aagaagcttc caaaacgtca tgaataaata tcatttctcaa      60
agcgttttag aggtcggcaa aattgggatt gtgattatct ttgcgcccat agtacggaat      120
gtacatcaac aacccctttt ttttaagccat aaatcaatta tgcgtattgt cagtaatttt      180
ttgttcgtct ctttttcggt tttgtttttt gcatcatgcc gttcccagcg agaaaaggtc      240
gtttacctgc aagatatcca aacttttaat cgggagatta tcgctaaacc atatgacgta      300
aaaattgaga aggacgatgt gctgaacatc cttgtcagca gtagagaccc ggagctttca      360
acgccctaca accaagtgtt gaccactcgt gcactggccc gcaacggcta tggaacgaac      420
tcgaacgaag gcttcctggg cgattcgaaa ggggtacatca attatcctat tttaggccag      480
atctatgtag agggccttac tcgtaccgaa ctggagaagg agatacagaa gaggattatt      540
tccagtggat ttatcaagga tcctacggta acggtgcagc ttcaaaattt caaggtgtcg      600
gttttgggag aggtgaatca tccgggttcg atgtcggtaa aaggagagcg aataactctt      660
ttggaagcga tcggaatggc cggagacctg acaatctatg gtcgccgcga tcgggttttt      720
gtgattagag aaaccgatgg gcatcgcgag gttttccaga cggatctcag aaaggccgac      780
ttgctcgcaa gcccgtgta ctatctgcat cagaacgacg tcatctatgt ggagccgaac      840
gacaagaaaa cacagatgag cgagatcaac cagaataata acgtaaactg atggctgagt      900
gttacctcca ctttggatc catttccacg ctgacgatta cgataataga taagaccaa
960

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(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...1338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

aaccccaaaaa	aagcccttgc	acttaatctg	aaaggaaaac	cgctgcccga	gatgctggcc	60
gaaccggccc	aaagtcctac	ttacgcggtc	gtgcccgcag	attttgaagg	tggtatcccc	120
aaggtgacgg	ctcgtccggg	ggataaggtg	cgtgccggct	cagcaatgat	gcaccacaag	180
gcataatccg	agatgaagtt	tacaagtcgg	gttagcggcg	aagtgatcgc	ggtgaatcgc	240
ggtgccaagc	gcaaggtgtt	gagcatcgag	gtgaaaccgg	acggactgaa	cgaatacgag	300
tcattccctg	tccgggatcc	gtctgccctc	tctgccgaac	agatcaagga	gcttttactg	360
tcgagcggta	tgtggggttt	tattaagcaa	cgctccttac	acatagtggc	tacaccggat	420
atagctccac	gcgacattta	tattactgcc	aactttactg	caccattggc	tccggacttc	480
gatttcacgc	ttcgaggaga	agaacgcggc	ctgcagactg	ccatcgatgc	cttggccaaa	540
ctcacgacag	gaaaggtgta	tgtgggcctg	aagccggggt	catctctggg	cttgacacaat	600
gcagaaatcg	tagaagtaca	cggacctcat	ccggcaggta	acgtgggctg	gctgatcaat	660
catacgaagc	caatcaatcg	gggcgaaaac	gtgtggacgc	tcaaggctac	cgacctgac	720
gtgatcggac	gtttcctgct	tacgggcaaa	gccgatttta	ccagaatgat	tgccatgacc	780
ggctcagacg	ctgcagctca	cggatacgtc	cgtattatgc	cgggttgcaa	tgtctttgct	840
tccttccccc	gccgactgac	aataaaggaa	tctcacgagc	gtgtgatcga	tggcaatgtg	900
ctgaccggta	agaagctctg	cgagaaggag	cctttcctgt	cagcccgggt	tgaccagatc	960
acggtgatcc	ccgaaggcga	cgatgtggac	gaactcttcg	ggtgggctgc	accccgtctc	1020
gatcagtaca	gcatagacag	agcttatttc	tcttggttgc	aggggaaaaa	caaagagtac	1080
gtactcgatg	cccggatcaa	gggtggcgaa	cgtgctatga	tcatagagcaa	cgagtatgac	1140
cgcgttttcc	cgatggacat	ctatccggag	tatttgctca	aggctattat	agcattcgac	1200
atcgacaaga	tggaggactt	aggcatatat	gaagtggctc	cggaggactt	tgccacttgc	1260
gaatttgtgg	atacatccaa	gatcgagctg	cagcgtatcg	ttcgcgaggg	cttggtatag	1320
ctctataagg	aatgaat					1338

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

aaccttagga	cacagccttt	cttttttgga	gatttgcaat	ctatgatcag	aacgatactt	60
tcacgatatg	tatcctcgaa	cttttggagt	cggggagcta	cctttttttt	caagattttc	120
ccggccttca	tctcgcgcgc	tactgctttg	ccggccttg	gaggggggtac	tgcttcaggc	180
tccgatcgta	cgctggctgt	gaccatcgag	ccacagaaat	acttcacga	gtccattg	240
gataagtcgg	tgcaggtggt	ggcattggta	ccggccggca	gcaatccgga	ggaatacgac	300
ccttcgccta	ccgtgatgaa	gcgtttgtcc	gaagcagatg	cctacttcta	tataggagga	360
ctgggggttcg	agcaaagaaa	tctcgtctgc	attcgggaca	ataaccctaa	gctccctctt	420
ttcgaaatgg	gcaaagcctt	ggcggatgcc	ggaagtgcag	atctccacgg	ctcctgcaca	480
gatcattctc	atacagacct	gcctgcccac	gatccgcact	attggagcag	tgtggtaggg	540
gcaaaggcac	tcagtcgtgc	tgcatacgac	gcgcttgtgg	agctttatcc	gaacgagaaa	600

gacaaatggg	acaaagggca	cgaccgtctc	aacggacgta	tcgacagcgt	gaagagactc	660
gtcgatacca	tgtttgccaa	tggttaaagca	gacaaagcct	tcgtcatata	tcacccatcg	720
ctcagctttt	tcgcccaga	gttcggcctg	cggcagatcg	tcatagagga	agatgggaaa	780
gagcctacgg	ctgcccacct	tcgtcgtgtg	atcgatcagg	cacgtgccga	tggtgtcaga	840
atcgtattta	tccaacccga	atttgaaacg	cgtcaggcgg	aggacatcgc	acgcgagatc	900
ggtgctcgtc	cggtaaggat	caatcctctg	cgcagctcgt	gggaggagga	aattttacat	960
attgctcgcg	ctttggctca	tgaacgg				987

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

tgctgcgcaa	ggcttcggga	cacctctccc	cggagaaggt	cgtttcggaa	tgataccggt	60
tttcocttatt	tcgttattca	tctgatcaaa	catattatca	ttatgacgga	caacaaacaa	120
cgtaatatcg	tattcccggc	gtttctcctc	ttgctgggag	tcatcgaggt	ggtgacgac	180
ggttggtttt	tcattgctcag	accggccgag	gagattatcc	aaggacagat	agaagtggcc	240
gaataccgag	tgccagcaa	agtgcgcggg	cgcattcaagg	aacttagggg	atccgagggg	300
cagcaggtgc	aggccggcga	taccctcgct	gtcatcgaag	cccccgacgt	agcgggctaag	360
atggagcagg	caaaggctgc	cgaagcagct	gcacaggctc	agaacgccaa	ggctctcaaa	420
ggagcacgca	gcgaacagat	acaggcagcc	tatgagatgt	ggcagaaagc	tcaggccggc	480
gtagccatag	cgaccaagac	acaccagcgc	gtgcagaacc	tctatgacca	gggagtggta	540
ccggctcaga	agttggacga	agccactgcc	cagcgcgatg	cggccatcgc	tacgcaaaaa	600
gcggccgaag	cccagtaaaa	tatggctcgc	aacgggtgccg	aacgcgaaga	caagctggca	660
gcttctgccc	tcgtcgatag	agcgagagga	gccgtcgccg	aggtggagtc	gtacatcaac	720
gaaacctacc	tcattcgcccc	acgggcaggc	gaagtgtcgg	agatattccc	caaagccggc	780
gaactcgtag	gtaccggcgc	acctatcatg	aatatcgccg	agatggggcg	tatgtgggccc	840
agctttgccc	ttcgtgagga	tttctctcagc	agcatgacca	tgggagccgt	tctggagact	900
gtggtgccgg	ctctgaatga	agaaaaagta	cgcttcaaga	tcacattcat	caagaacatg	960
ggtacctatg	ctgcctggaa	agcgaccaag	acaacagggc	agtacgacct	gaagaccttc	1020
gaggtaaagg	ccacccttgc	ggataaagac	aaggcacaaa	agctacgccc	gggtatgtcc	1080
gtgatcatat	gcaag					1095

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

acgaataaaa	aagaagagac	aatgaagaaa	tcaagtgtag	tagcctcagt	tttggccgtg	60
gctctcgtgt	tcgccggttg	cggactgaac	aatatggcaa	aaggcggcct	tatcggcgcc	120
ggagtaggag	gtgccattgg	tgccggagta	ggtaacgtag	cgggaaatac	ggctgtcggg	180
gccatcgtcg	gtactgcagt	cgggtggagca	gccggtgctc	tcatcggaaa	gaagatggac	240
aagcagaaaa	aagaactgga	ggccgcagta	cccgatgcta	cgattcagac	agtaaatac	300
ggagaggcta	ttctgggttac	tttcgatagc	ggtatcctct	ttgcgacgaa	ctccagcact	360
ctgagtccca	actcacgcac	tgcgctgacg	aagtttgctg	caaacatgaa	caaaaacccc	420
gacacggata	ttcgtatcgt	aggccatacg	gacaataccg	gctccgacaa	gatcaacgat	480
cctctgtctg	agagacgtgc	agccagcgta	tattctttcc	tgaattctca	gggtgtgagt	540
atgtcgcgca	tggcagccga	agggcgtggg	agccatgaac	cggttgcaga	caatagcaca	600
gttgccggac	gttcggccaa	ccgccgtgtg	gaggtttata	tcttgccgaa	tgccaagatg	660
atcgaacaag	cacagcaagg	tacgctgaag	taa			693

(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

gaaggggcca	gcttcgtcct	tgctctcacc	ggcaagggct	tcgtgccggc	tcgtctcttg	60
gagcgcgtga	acgaggctct	cgaaaaagac	gaaatcgtaa	agggctatgt	gaagtgtcgt	120
accaaggggtg	gtatgatcgt	cgatgtattc	ggtatcgagg	ctttcctccc	gggatcacag	180
atcgacgtgc	gccccattcg	cgactacgat	gcattcgttg	agaagacgat	ggagttcaag	240
attgtgaaaa	tcaatcaaga	atataagaat	gtagttgttt	cccacaagg	gctcatcgaa	300
gcagagctcg	aacaacagaa	gaaagaaatc	atcggcaagc	tcgaaaaagg	gcagggtactc	360
gaagggtatcg	tcaagaatat	tacttcttac	ggagtattta	tcgacctcgg	tggagtggat	420
ggtcttatcc	atatcactga	cctttcatgg	ggtcgtgtgg	ctcatccgga	agaaatcgta	480
cagctggatc	agaagatcaa	tgctcgttatc	ctcgactttg	atgaagatcg	caagcgtatc	540
gctctcggac	tcaaacagct	gatgcctcat	ccttgggatg	ctctcgacag	cgagcttaag	600
gtaggcgata	aggtgaagg	taaagttgtg	gtgatggcag	attacggtgc	tttcgttgag	660

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attgcacagg gcgttgaggg tcttatccac gtaagcgaaa tgtcatggac acagcacttg 720
cggtctgctc aggacttccct gcatgtaggc gacgaagtgg aagccgtgat cctgacgctc 780
gaccgcgaag aacgcaaaat gtcgctcggt ctgaagcaac tcaagccgga tccttgggct 840
gatatcgaaa ctggtttccc tgtaggctct cgtcaccatg ctggtgttcg caacttcacc 900
aatttcggtg tattcgttga gatcgaagag ggcgtagatg gccttatcca tatttccgac 960
ctttcttgga cgaagaagat caaacacccc agcgagttta cggaagtagg tgctgatatc 1020
gaagttcagg taatcgagat cgacaaggaa aaccgtcgtc tcagcttggg tcacaaacag 1080
ttggaagaga atccttggga tgtattcgag acggtattca ctgtaggata tatccacgaa 1140
ggaacggtaa tcgaagtgat ggacaagggt gctgtcgttt ctctgcctta cgggtgtggaa 1200
ggttttgcca ctccgaagca catggtgaag gaagatggct cacaggctgt actcgaagag 1260
aagttacett tcaaggttat tgagttcaat aaggatgcc aagcaatcat tgtatctcat 1320
agccgtgtat tcgaagatga gcagaaaatg gctcagcgtg aagccaatgc agagcgtaag 1380
gctgaagcca aagcggctca gaaagaagct gctgccgaag ctgccaatcc tgcacaggct 1440
gtagagaaaag ccactctcgg agacctcggc gagctggccg ctttgaaaga aaagctttca 1500
gaaaac

```

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

```

Pro Gln Ser Ser Pro Asp Arg Arg Ser Phe Gln Asn Val Met Asn Lys
1          5          10          15
Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly Ile Val Ile
          20          25          30
Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro Pro Phe Leu
          35          40          45
Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu Phe Val Ser
          50          55          60
Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg Glu Lys Val
          65          70          75          80
Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile Ile Ala Lys
          85          90          95
Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn Ile Leu Val
          100         105         110
Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln Val Leu Thr
          115         120         125
Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser Asn Glu Gly
          130         135         140
Phe Leu Val Asp Ser Lys Gly Tyr Il Asn Tyr Pro Ile Leu Gly Gln
          145         150         155         160
Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys Glu Ile Gln
          165         170         175
Lys Arg Ile Ile S r Ser Gly Phe Ile Lys Asp Pro Thr Val Thr Val
          180         185         190
Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val Asn His Pro

```


195	200	205
Gly Ser Met Ser Val Lys	Gly Glu Arg Ile Thr	Leu Leu Glu Ala Ile
210	215	220
Gly Met Ala Gly Asp Leu	Thr Ile Tyr Gly Arg Arg	Asp Arg Val Phe
225	230	235
Val Ile Arg Glu Thr Asp	Gly His Arg Glu Val Ph	Gln Thr Asp Leu
245	250	255
Arg Lys Ala Asp Leu Leu	Ala Ser Pro Val Tyr Tyr	Leu His Gln Asn
260	265	270
Asp Val Ile Tyr Val Glu	Pro Asn Asp Lys Lys Thr	Gln Met Ser Glu
275	280	285
Ile Asn Gln Asn Asn Asn	Val Asn Val Trp Leu Ser	Val Thr Ser Thr
290	295	300
Leu Val Ser Ile Ser Thr	Leu Thr Ile Thr Ile	Ile Asp Lys Thr Lys
305	310	315
		320

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

Asn Pro Lys Lys Ala Leu Ala Leu Asn Leu Lys Gly Lys Pro Leu Pro	1	5	10	15
Glu Met Leu Ala Glu Pro Ala Gln Ser Pro Thr Tyr Ala Val Val Pro	20	25	30	
Asp Asp Phe Glu Gly Val Ile Pro Lys Val Thr Ala Arg Pro Gly Asp	35	40	45	
Lys Val Arg Ala Gly Ser Ala Leu Met His His Lys Ala Tyr Pro Glu	50	55	60	
Met Lys Phe Thr Ser Pro Val Ser Gly Glu Val Ile Ala Val Asn Arg	65	70	75	80
Gly Ala Lys Arg Lys Val Leu Ser Ile Glu Val Lys Pro Asp Gly Leu	85	90	95	
Asn Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro Ser Ala Leu Ser Ala	100	105	110	
Glu Gln Ile Lys Glu Leu Leu Leu Ser Ser Gly Met Trp Gly Phe Ile	115	120	125	
Lys Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro Asp Ile Ala Pro Arg	130	135	140	
Asp Il Tyr Ile Thr Ala Asn Phe Thr Ala Pro L u Ala Pro Asp Phe	145	150	155	160
Asp Phe Ile Val Arg Gly Glu Glu Arg Ala Leu Gln Thr Ala Ile Asp	165	170	175	
Ala Leu Ala Lys Leu Thr Thr Gly Lys Val Tyr Val Gly Leu Lys Pro	180	185	190	
Gly Ser Ser Leu Gly Leu His Asn Ala Glu Ile Val Glu Val His Gly				

```

195          200          205
Pro His Pro Ala Gly Asn Val Gly Val Leu Ile Asn His Thr Lys Pro
210          215          220
Ile Asn Arg Gly Glu Thr Val Trp Thr Leu Lys Ala Thr Asp Leu Il
225          230          235          240
Val Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala Asp Phe Thr Arg Met
245          250          255
Ile Ala Met Thr Gly Ser Asp Ala Ala Ala His Gly Tyr Val Arg Ile
260          265          270
Met Pro Gly Cys Asn Val Phe Ala Ser Phe Pro Gly Arg Leu Thr Ile
275          280          285
Lys Glu Ser His Glu Arg Val Ile Asp Gly Asn Val Leu Thr Gly Lys
290          295          300
Lys Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala Arg Cys Asp Gln Ile
305          310          315          320
Thr Val Ile Pro Glu Gly Asp Asp Val Asp Glu Leu Phe Gly Trp Ala
325          330          335
Ala Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg Ala Tyr Phe Ser Trp
340          345          350
Leu Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp Ala Arg Ile Lys Gly
355          360          365
Gly Glu Arg Ala Met Ile Met Ser Asn Glu Tyr Asp Arg Val Phe Pro
370          375          380
Met Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala Ile Ile Ala Phe Asp
385          390          395          400
Ile Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu Val Ala Pro Glu Asp
405          410          415
Phe Ala Thr Cys Glu Phe Val Asp Thr Ser Lys Ile Glu Leu Gln Arg
420          425          430
Ile Val Arg Glu Gly Leu Asp Met Leu Tyr Lys Glu Met Asn
435          440          445

```

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

```

Asn Leu Arg Thr Gln Pro Phe Phe Leu Val Asp Leu Gln Ser Met Ile
1          5          10          15
Arg Thr Il  Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser Arg Gly
20          25          30
Ala Thr Phe Phe Ph  Thr Ile Ph  Pro Ala Phe Ile Leu Ala Ala Thr
35          40          45
Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp Arg Thr
50          55          60
Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser Ile Ala

```

18
 65 70 75 80
 Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser Asn Pro
 85 90 95
 Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser Glu Ala
 100 105 110
 Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg Asn Leu
 115 120 125
 Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu Met Gly
 130 135 140
 Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser Cys Thr
 145 150 155 160
 Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr Trp Ser
 165 170 175
 Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp Ala Leu
 180 185 190
 Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly His Asp
 195 200 205
 Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp Thr Met
 210 215 220
 Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His Pro Ser
 225 230 235 240
 Leu Ser Phe Phe Ala Gln Glu Phe Gly Leu Arg Gln Ile Val Ile Glu
 245 250 255
 Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val Ile Asp
 260 265 270
 Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro Glu Phe
 275 280 285
 Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala Arg Pro
 290 295 300
 Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile Leu His
 305 310 315 320
 Ile Ala Arg Ala Leu Ala His Glu Arg
 325

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Cys Cys Ala Arg Leu Arg Asp Thr Ser Pro Arg Lys Lys Ser Ph Arg
 1 5 10 15
 Asn Asp Thr Val Phe Pro Tyr Phe Val Ile His L u Ile Lys His Ile
 20 25 30
 Il Ile M t Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe
 35 40 45
 Leu Leu L u L u Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe

50		55		60	
Met	Leu	Arg	Pro	Ala	Glu
65					70
Glu	Tyr	Arg	Val	Ser	Ser
				85	
Val	Ser	Glu	Gly	Gln	Gln
				100	
Glu	Ala	Pro	Asp	Val	Ala
				115	
Ala	Ala	Ala	Gln	Ala	Gln
				130	
Glu	Gln	Ile	Gln	Ala	Ala
145				150	
Val	Ala	Ile	Ala	Thr	Lys
				165	
Gln	Gly	Val	Val	Pro	Ala
				180	
Asp	Ala	Ala	Ile	Ala	Thr
				195	
Ala	Arg	Asn	Gly	Ala	Glu
210				215	
Val	Asp	Arg	Ala	Arg	Gly
225				230	
Glu	Thr	Tyr	Leu	Ile	Ala
				245	
Pro	Lys	Ala	Gly	Glu	Leu
				260	
Ala	Glu	Met	Gly	Asp	Met
				275	
Leu	Ser	Ser	Met	Thr	Met
290				295	
Leu	Asn	Glu	Glu	Lys	Val
305				310	
Gly	Thr	Tyr	Ala	Ala	Trp
				325	
Leu	Lys	Thr	Phe	Glu	Val
				340	
Gln	Lys	Leu	Arg	Pro	Gly
				355	
					360
					365

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_f atur
- (B) LOCATION 1...230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Thr Asn Lys Lys Glu Glu Thr Met Lys Lys Ser Ser Val Val Ala Ser

				5					10					15			
Val	Leu	Ala	Val	Ala	Leu	Val	Phe	Ala	Gly	Cys	Gly	Leu	Asn	Asn	Met		
			20					25					30				
Ala	Lys	Gly	Gly	Leu	Ile	Gly	Ala	Gly	Val	Gly	Gly	Ala	Ile	Gly	Ala		
		35					40					45					
Gly	Val	Gly	Asn	Val	Ala	Gly	Asn	Thr	Ala	Val	Gly	Ala	Ile	Val	Gly		
		50				55					60						
Thr	Ala	Val	Gly	Gly	Ala	Ala	Gly	Ala	Leu	Ile	Gly	Lys	Lys	Met	Asp		
65					70				75						80		
Lys	Gln	Lys	Lys	Glu	Leu	Glu	Ala	Ala	Val	Pro	Asp	Ala	Thr	Ile	Gln		
			85						90					95			
Thr	Val	Asn	Asp	Gly	Glu	Ala	Ile	Leu	Val	Thr	Phe	Asp	Ser	Gly	Ile		
		100						105					110				
Leu	Phe	Ala	Thr	Asn	Ser	Ser	Thr	Leu	Ser	Pro	Asn	Ser	Arg	Thr	Ala		
		115					120					125					
Leu	Thr	Lys	Phe	Ala	Ala	Asn	Met	Asn	Lys	Asn	Pro	Asp	Thr	Asp	Ile		
		130				135					140						
Arg	Ile	Val	Gly	His	Thr	Asp	Asn	Thr	Gly	Ser	Asp	Lys	Ile	Asn	Asp		
145					150					155					160		
Pro	Leu	Ser	Glu	Arg	Arg	Ala	Ala	Ser	Val	Tyr	Ser	Phe	Leu	Asn	Ser		
			165					170					175				
Gln	Gly	Val	Ser	Met	Ser	Arg	Met	Ala	Ala	Glu	Gly	Arg	Gly	Ser	His		
		180					185						190				
Glu	Pro	Val	Ala	Asp	Asn	Ser	Thr	Val	Ala	Gly	Arg	Ser	Ala	Asn	Arg		
		195				200					205						
Arg	Val	Glu	Val	Tyr	Ile	Leu	Pro	Asn	Ala	Lys	Met	Ile	Glu	Gln	Ala		
		210				215					220						
Gln	Gln	Gly	Thr	Leu	Lys												
225					230												

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Glu	Gly	Ala	Ser	Phe	Val	Leu	Val	Leu	Thr	Gly	Lys	Gly	Phe	Val	Pro		
1				5				10					15				
Ala	Arg	Ser	Trp	Glu	Arg	Val	Asn	Glu	Ala	Leu	Glu	Lys	Asp	Glu	Ile		
		20					25					30					
Val	Lys	Gly	Tyr	Val	Lys	Cys	Arg	Thr	Lys	Gly	Gly	Met	Ile	Val	Asp		
		35				40					45						
Val	Phe	Gly	Ile	Glu	Ala	Phe	Leu	Pro	Gly	Ser	Gln	Ile	Asp	Val	Arg		
		50				55					60						
Pro	Ile	Arg	Asp	Tyr	Asp	Ala	Phe	Val	Glu	Lys	Thr	Met	Glu	Phe	Lys		
65				70					75						80		
Ile	Val	Lys	Ile	Asn	Gln	Glu	Tyr	Lys	Asn	Val	Val	Val	Ser	His	Lys		

				85					90					95	
Val	Leu	Ile	Glu	Ala	Glu	Leu	Glu	Gln	Gln	Lys	Lys	Glu	Ile	Ile	Gly
			100					105					110		
Lys	Leu	Glu	Lys	Gly	Gln	Val	Leu	Glu	Gly	Ile	Val	Lys	Asn	Ile	Thr
			115					120					125		
Ser	Tyr	Gly	Val	Phe	Ile	Asp	Leu	Gly	Gly	Val	Asp	Gly	Leu	Ile	His
			130				135					140			
Ile	Thr	Asp	Leu	Ser	Trp	Gly	Arg	Val	Ala	His	Pro	Glu	Glu	Ile	Val
						150					155				160
Gln	Leu	Asp	Gln	Lys	Ile	Asn	Val	Val	Ile	Leu	Asp	Phe	Asp	Glu	Asp
				165					170					175	
Arg	Lys	Arg	Ile	Ala	Leu	Gly	Leu	Lys	Gln	Leu	Met	Pro	His	Pro	Trp
				180					185				190		
Asp	Ala	Leu	Asp	Ser	Glu	Leu	Lys	Val	Gly	Asp	Lys	Val	Lys	Gly	Lys
			195				200					205			
Val	Val	Val	Met	Ala	Asp	Tyr	Gly	Ala	Phe	Val	Glu	Ile	Ala	Gln	Gly
			210				215					220			
Val	Glu	Gly	Leu	Ile	His	Val	Ser	Glu	Met	Ser	Trp	Thr	Gln	His	Leu
					230					235					240
Arg	Ser	Ala	Gln	Asp	Phe	Leu	His	Val	Gly	Asp	Glu	Val	Glu	Ala	Val
				245					250					255	
Ile	Leu	Thr	Leu	Asp	Arg	Glu	Glu	Arg	Lys	Met	Ser	Leu	Gly	Leu	Lys
			260					265					270		
Gln	Leu	Lys	Pro	Asp	Pro	Trp	Ala	Asp	Ile	Glu	Thr	Arg	Phe	Pro	Val
			275				280					285			
Gly	Ser	Arg	His	His	Ala	Arg	Val	Arg	Asn	Phe	Thr	Asn	Phe	Gly	Val
			290				295				300				
Phe	Val	Glu	Ile	Glu	Glu	Gly	Val	Asp	Gly	Leu	Ile	His	Ile	Ser	Asp
					310					315					320
Leu	Ser	Trp	Thr	Lys	Lys	Ile	Lys	His	Pro	Ser	Glu	Phe	Thr	Glu	Val
				325					330					335	
Gly	Ala	Asp	Ile	Glu	Val	Gln	Val	Ile	Glu	Ile	Asp	Lys	Glu	Asn	Arg
			340					345					350		
Arg	Leu	Ser	Leu	Gly	His	Lys	Gln	Leu	Glu	Glu	Asn	Pro	Trp	Asp	Val
			355				360					365			
Phe	Glu	Thr	Val	Phe	Thr	Val	Gly	Ser	Ile	His	Glu	Gly	Thr	Val	Ile
			370				375				380				
Glu	Val	Met	Asp	Lys	Gly	Ala	Val	Val	Ser	Leu	Pro	Tyr	Gly	Val	Glu
					390					395					400
Gly	Phe	Ala	Thr	Pro	Lys	His	Met	Val	Lys	Glu	Asp	Gly	Ser	Gln	Ala
				405					410					415	
Val	Leu	Glu	Glu	Lys	Leu	Pro	Phe	Lys	Val	Ile	Glu	Phe	Asn	Lys	Asp
				420				425					430		
Ala	Lys	Arg	Ile	Ile	Val	Ser	His	Ser	Arg	Val	Phe	Glu	Asp	Glu	Gln
			435				440					445			
Lys	Met	Ala	Gln	Arg	Glu	Ala	Asn	Ala	Glu	Arg	Lys	Ala	Glu	Ala	Lys
					455						460				
Ala	Ala	Gln	Lys	Glu	Ala	Ala	Ala	Glu	Ala	Ala	Asn	Pro	Ala	Gln	Ala
					470					475					480
Val	Glu	Lys	Ala	Thr	Leu	Gly	Asp	Leu	Gly	Glu	Leu	Ala	Ala	Leu	Lys
				485					490					495	
Glu	Lys	Leu	Ser	Glu	Asn										
				500											

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

```

Met Asn Lys Tyr His Ser Gln Ser Val Leu Glu Val Gly Lys Ile Gly
1      5      10      15
Ile Val Ile Ile Phe Ala Pro Ile Val Arg Asn Val His Gln Gln Pro
20     25     30
Pro Phe Leu Ser His Lys Ser Ile Met Arg Ile Val Ser Asn Phe Leu
35     40     45
Phe Val Ser Phe Ser Val Leu Leu Phe Ala Ser Cys Arg Ser Gln Arg
50     55     60
Glu Lys Val Val Tyr Leu Gln Asp Ile Gln Thr Phe Asn Arg Glu Ile
65     70     75     80
Ile Ala Lys Pro Tyr Asp Val Lys Ile Glu Lys Asp Asp Val Leu Asn
85     90     95
Ile Leu Val Ser Ser Arg Asp Pro Glu Leu Ser Thr Pro Tyr Asn Gln
100    105    110
Val Leu Thr Thr Arg Ala Leu Ala Arg Asn Gly Tyr Gly Thr Asn Ser
115    120    125
Asn Glu Gly Phe Leu Val Asp Ser Lys Gly Tyr Ile Asn Tyr Pro Ile
130    135    140
Leu Gly Gln Ile Tyr Val Glu Gly Leu Thr Arg Thr Glu Leu Glu Lys
145    150    155    160
Glu Ile Gln Lys Arg Ile Ile Ser Ser Gly Phe Ile Lys Asp Pro Thr
165    170    175
Val Thr Val Gln Leu Gln Asn Phe Lys Val Ser Val Leu Gly Glu Val
180    185    190
Asn His Pro Gly Ser Met Ser Val Lys Gly Glu Arg Ile Thr Leu Leu
195    200    205
Glu Ala Ile Gly Met Ala Gly Asp Leu Thr Ile Tyr Gly Arg Arg Asp
210    215    220
Arg Val Phe Val Ile Arg Glu Thr Asp Gly His Arg Glu Val Phe Gln
225    230    235    240
Thr Asp Leu Arg Lys Ala Asp Leu Leu Ala Ser Pro Val Tyr Tyr Leu
245    250    255
His Gln Asn Asp Val Ile Tyr Val Glu Pro Asn Asp Lys Lys Thr Gln
260    265    270
Met Ser Glu Ile Asn Gln Asn Asn Val Asn Val Trp Leu Ser Val
275    280    285
Thr Ser Thr Leu Val Ser Ile Ser Thr Leu Thr Ile Thr Ile Ile Asp
290    295    300
Lys Thr Lys
305

```

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Porphyromonas gingivalis*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...429
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```

Met Leu Ala Glu Pro Ala Gln Ser Pro Thr Tyr Ala Val Val Pro Asp
1      5      10      15
Asp Phe Glu Gly Val Ile Pro Lys Val Thr Ala Arg Pro Gly Asp Lys
20      25      30
Val Arg Ala Gly Ser Ala Leu Met His His Lys Ala Tyr Pro Glu Met
35      40      45
Lys Phe Thr Ser Pro Val Ser Gly Glu Val Ile Ala Val Asn Arg Gly
50      55      60
Ala Lys Arg Lys Val Leu Ser Ile Glu Val Lys Pro Asp Gly Leu Asn
65      70      75      80
Glu Tyr Glu Ser Phe Pro Val Gly Asp Pro Ser Ala Leu Ser Ala Glu
85      90      95
Gln Ile Lys Glu Leu Leu Leu Ser Ser Gly Met Trp Gly Phe Ile Lys
100     105     110
Gln Arg Pro Tyr Asp Ile Val Ala Thr Pro Asp Ile Ala Pro Arg Asp
115     120     125
Ile Tyr Ile Thr Ala Asn Phe Thr Ala Pro Leu Ala Pro Asp Phe Asp
130     135     140
Phe Ile Val Arg Gly Glu Glu Arg Ala Leu Gln Thr Ala Ile Asp Ala
145     150     155     160
Leu Ala Lys Leu Thr Gly Lys Val Tyr Val Gly Leu Lys Pro Gly
165     170     175
Ser Ser Leu Gly Leu His Asn Ala Glu Ile Val Glu Val His Gly Pro
180     185     190
His Pro Ala Gly Asn Val Gly Val Leu Ile Asn His Thr Lys Pro Ile
195     200     205
Asn Arg Gly Glu Thr Val Trp Thr Leu Lys Ala Thr Asp Leu Ile Val
210     215     220
Ile Gly Arg Phe Leu Leu Thr Gly Lys Ala Asp Phe Thr Arg Met Ile
225     230     235     240
Ala Met Thr Gly Ser Asp Ala Ala Ala His Gly Tyr Val Arg Ile Met
245     250     255
Pro Gly Cys Asn Val Phe Ala Ser Phe Pro Gly Arg Leu Thr Ile Lys
260     265     270
Glu Ser His Glu Arg Val Ile Asp Gly Asn Val Leu Thr Gly Lys Lys
275     280     285
Leu Cys Glu Lys Glu Pro Phe Leu Ser Ala Arg Cys Asp Gln Ile Thr
290     295     300
Val Ile Pro Glu Gly Asp Asp Val Asp Glu Leu Phe Gly Trp Ala Ala
305     310     315     320
Pro Arg Leu Asp Gln Tyr Ser Met Ser Arg Ala Tyr Phe Ser Trp Leu
325     330     335
Gln Gly Lys Asn Lys Glu Tyr Val Leu Asp Ala Arg Ile Lys Gly Gly
340     345     350
Glu Arg Ala Met Ile Met Ser Asn Glu Tyr Asp Arg Val Phe Pro Met
355     360     365
Asp Ile Tyr Pro Glu Tyr Leu Leu Lys Ala Ile Ile Ala Phe Asp Ile

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          370          375          380
Asp Lys Met Glu Asp Leu Gly Ile Tyr Glu Val Ala Pro Glu Asp Phe
385          390          395          400
Ala Thr Cys Glu Phe Val Asp Thr Ser Lys Ile Glu Leu Gln Arg Ile
          405          410          415
Val Arg Glu Gly Leu Asp Met Leu Tyr Lys Glu Met Asn
          420          425

```

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```

Met Ile Arg Thr Ile Leu Ser Arg Tyr Val Ser Ser Asn Phe Trp Ser
1          5          10          15
Arg Gly Ala Thr Phe Phe Phe Thr Ile Phe Pro Ala Phe Ile Leu Ala
          20          25          30
Ala Thr Ala Leu Pro Ala Cys Gly Gly Gly Thr Ala Ser Gly Ser Asp
          35          40          45
Arg Thr Leu Ala Val Thr Ile Glu Pro Gln Lys Tyr Phe Ile Glu Ser
          50          55          60
Ile Ala Asp Lys Ser Val Gln Val Val Ala Leu Val Pro Ala Gly Ser
65          70          75          80
Asn Pro Glu Glu Tyr Asp Pro Ser Pro Thr Val Met Lys Arg Leu Ser
          85          90          95
Glu Ala Asp Ala Tyr Phe Tyr Ile Gly Gly Leu Gly Phe Glu Gln Arg
          100          105          110
Asn Leu Ala Ala Ile Arg Asp Asn Asn Pro Lys Leu Pro Leu Phe Glu
          115          120          125
Met Gly Lys Ala Leu Ala Asp Ala Gly Ser Ala Asp Leu His Gly Ser
          130          135          140
Cys Thr Asp His Ser His Thr Asp Leu His Ala His Asp Pro His Tyr
145          150          155          160
Trp Ser Ser Val Val Gly Ala Lys Ala Leu Ser Arg Ala Ala Tyr Asp
          165          170          175
Ala Leu Val Glu Leu Tyr Pro Asn Glu Lys Asp Lys Trp Asp Lys Gly
          180          185          190
His Asp Arg Leu Asn Gly Arg Ile Asp Ser Val Lys Arg Leu Val Asp
          195          200          205
Thr Met Phe Ala Asn Gly Lys Ala Asp Lys Ala Phe Val Ile Tyr His
          210          215          220
Pro S r L u Ser Phe Phe Ala Gln Glu Ph Gly Leu Arg Gln Ile Val
225          230          235          240
Ile Glu Glu Asp Gly Lys Glu Pro Thr Ala Ala His Leu Arg Arg Val
          245          250          255
Il Asp Gln Ala Arg Ala Asp Gly Val Arg Ile Val Phe Ile Gln Pro

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                260                265                270
Glu Phe Glu Thr Arg Gln Ala Glu Asp Ile Ala Arg Glu Ile Gly Ala
                275                280                285
Arg Pro Val Arg Ile Asn Pro Leu Arg Ser Ser Trp Glu Glu Glu Ile
                290                295                300
Leu His Ile Ala Arg Ala Leu Ala His Glu Arg
305                310                315

```

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

```

Met Thr Asp Asn Lys Gln Arg Asn Ile Val Phe Pro Ala Phe Leu Leu
1          5          10          15
Leu Leu Gly Val Ile Ala Val Val Thr Ile Val Gly Phe Phe Met Leu
20          25          30
Arg Pro Ala Glu Glu Ile Ile Gln Gly Gln Ile Glu Val Thr Glu Tyr
35          40          45
Arg Val Ser Ser Lys Val Pro Gly Arg Ile Lys Glu Leu Arg Val Ser
50          55          60
Glu Gly Gln Gln Val Gln Ala Gly Asp Thr Leu Ala Val Ile Glu Ala
65          70          75          80
Pro Asp Val Ala Ala Lys Met Glu Gln Ala Lys Ala Ala Glu Ala Ala
85          90          95
Ala Gln Ala Gln Asn Ala Lys Ala Leu Lys Gly Ala Arg Ser Glu Gln
100         105         110
Ile Gln Ala Ala Tyr Glu Met Trp Gln Lys Ala Gln Ala Gly Val Ala
115         120         125
Ile Ala Thr Lys Thr His Gln Arg Val Gln Asn Leu Tyr Asp Gln Gly
130         135         140
Val Val Pro Ala Gln Lys Leu Asp Glu Ala Thr Ala Gln Arg Asp Ala
145         150         155         160
Ala Ile Ala Thr Gln Lys Ala Ala Glu Ala Gln Tyr Asn Met Ala Arg
165         170         175
Asn Gly Ala Glu Arg Glu Asp Lys Leu Ala Ala Ser Ala Leu Val Asp
180         185         190
Arg Ala Arg Gly Ala Val Ala Glu Val Glu Ser Tyr Ile Asn Glu Thr
195         200         205
Tyr Leu Il Ala Pro Arg Ala Gly Glu Val Ser Glu Ile Phe Pro Lys
210         215         220
Ala Gly Glu Leu Val Gly Thr Gly Ala Pro Ile Met Asn Ile Ala Glu
225         230         235         240
Met Gly Asp Met Trp Ala Ser Phe Ala Val Arg Glu Asp Phe Leu Ser
245         250         255
Ser Met Thr Met Gly Ala Val Leu Glu Thr Val Val Pro Ala Leu Asn

```

	260		265		270										
Glu	Glu	Lys	Val	Arg	Phe	Lys	Ile	Thr	Phe	Ile	Lys	Asn	Met	Gly	Thr
	275		280		285										
Tyr	Ala	Ala	Trp	Lys	Ala	Thr	Lys	Thr	Thr	Gly	Gln	Tyr	Asp	Leu	Lys
	290		295		300										
Thr	Phe	Glu	Val	Lys	Ala	Thr	Leu	Ala	Asp	Lys	Asp	Lys	Ala	Gln	Lys
305			310		315				320						
Leu	Arg	Pro	Gly	Met	Ser	Val	Ile	Ile	Arg	Lys					
			325					330							

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

Met	Lys	Lys	Ser	Ser	Val	Val	Ala	Ser	Val	Leu	Ala	Val	Ala	Leu	Val
1			5					10						15	
Phe	Ala	Gly	Cys	Gly	Leu	Asn	Asn	Met	Ala	Lys	Gly	Gly	Leu	Ile	Gly
		20					25						30		
Ala	Gly	Val	Gly	Gly	Ala	Ile	Gly	Ala	Gly	Val	Gly	Asn	Val	Ala	Gly
		35				40						45			
Asn	Thr	Ala	Val	Gly	Ala	Ile	Val	Gly	Thr	Ala	Val	Gly	Gly	Ala	Ala
	50				55					60					
Gly	Ala	Leu	Ile	Gly	Lys	Lys	Met	Asp	Lys	Gln	Lys	Lys	Glu	Leu	Glu
65				70					75				80		
Ala	Ala	Val	Pro	Asp	Ala	Thr	Ile	Gln	Thr	Val	Asn	Asp	Gly	Glu	Ala
			85					90					95		
Ile	Leu	Val	Thr	Phe	Asp	Ser	Gly	Ile	Leu	Phe	Ala	Thr	Asn	Ser	Ser
		100					105						110		
Thr	Leu	Ser	Pro	Asn	Ser	Arg	Thr	Ala	Leu	Thr	Lys	Phe	Ala	Ala	Asn
		115				120						125			
Met	Asn	Lys	Asn	Pro	Asp	Thr	Asp	Ile	Arg	Ile	Val	Gly	His	Thr	Asp
	130					135				140					
Asn	Thr	Gly	Ser	Asp	Lys	Ile	Asn	Asp	Pro	Leu	Ser	Glu	Arg	Arg	Ala
145				150					155					160	
Ala	Ser	Val	Tyr	Ser	Phe	Leu	Asn	Ser	Gln	Gly	Val	Ser	Met	Ser	Arg
			165						170				175		
Met	Ala	Ala	Glu	Gly	Arg	Gly	Ser	His	Glu	Pro	Val	Ala	Asp	Asn	Ser
		180				185						190			
Thr	Val	Ala	Gly	Arg	Ser	Ala	Asn	Arg	Arg	Val	Glu	Val	Tyr	Ile	L u
		195				200						205			
Pro	Asn	Ala	Lys	M t	Ile	Glu	Gln	Ala	Gln	Gln	Gly	Thr	Leu	Lys	
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

```

Met Glu Phe Lys Ile Val Lys Ile Asn Gln Glu Tyr Lys Asn Val Val
1      5      10      15
Val Ser His Lys Val Leu Ile Glu Ala Glu Leu Glu Gln Gln Lys Lys
20      25      30
Glu Ile Ile Gly Lys Leu Glu Lys Gly Gln Val Leu Glu Gly Ile Val
35      40      45
Lys Asn Ile Thr Ser Tyr Gly Val Phe Ile Asp Leu Gly Gly Val Asp
50      55      60
Gly Leu Ile His Ile Thr Asp Leu Ser Trp Gly Arg Val Ala His Pro
65      70      75      80
Glu Glu Ile Val Gln Leu Asp Gln Lys Ile Asn Val Val Ile Leu Asp
85      90      95
Phe Asp Glu Asp Arg Lys Arg Ile Ala Leu Gly Leu Lys Gln Leu Met
100     105     110
Pro His Pro Trp Asp Ala Leu Asp Ser Glu Leu Lys Val Gly Asp Lys
115     120     125
Val Lys Gly Lys Val Val Val Met Ala Asp Tyr Gly Ala Phe Val Glu
130     135     140
Ile Ala Gln Gly Val Glu Gly Leu Ile His Val Ser Glu Met Ser Trp
145     150     155     160
Thr Gln His Leu Arg Ser Ala Gln Asp Phe Leu His Val Gly Asp Glu
165     170     175
Val Glu Ala Val Ile Leu Thr Leu Asp Arg Glu Glu Arg Lys Met Ser
180     185     190
Leu Gly Leu Lys Gln Leu Lys Pro Asp Pro Trp Ala Asp Ile Glu Thr
195     200     205
Arg Phe Pro Val Gly Ser Arg His His Ala Arg Val Arg Asn Phe Thr
210     215     220
Asn Phe Gly Val Phe Val Glu Ile Glu Glu Gly Val Asp Gly Leu Ile
225     230     235     240
His Ile Ser Asp Leu Ser Trp Thr Lys Lys Ile Lys His Pro Ser Glu
245     250     255
Phe Thr Glu Val Gly Ala Asp Ile Glu Val Gln Val Ile Glu Ile Asp
260     265     270
Lys Glu Asn Arg Arg Leu S r Leu Gly His Lys Gln Leu Glu Glu Asn
275     280     285
Pro Trp Asp Val Phe Glu Thr Val Ph Thr Val Gly Ser Ile His Glu
290     295     300
Gly Thr Val Il Glu Val M t Asp Lys Gly Ala Val Val Ser L u Pro
305     310     315     320
Tyr Gly Val Glu Gly Ph Ala Thr Pro Lys His Met Val Lys Glu Asp
325     330     335

```

Gly	Ser	Gln	Ala	Val	Leu	Glu	Glu	Lys	Leu	Pro	Phe	Lys	Val	Ile	Glu
			340					345					350		
Phe	Asn	Lys	Asp	Ala	Lys	Arg	Ile	Ile	Val	Ser	His	Ser	Arg	Val	Phe
		355					360					365			
Glu	Asp	Glu	Gln	Lys	Met	Ala	Gln	Arg	Glu	Ala	Asn	Ala	Glu	Arg	Lys
	370					375					380				
Ala	Glu	Ala	Lys	Ala	Ala	Gln	Lys	Glu	Ala	Ala	Ala	Glu	Ala	Ala	Asn
385					390					395					400
Pro	Ala	Gln	Ala	Val	Glu	Lys	Ala	Thr	Leu	Gly	Asp	Leu	Gly	Glu	Leu
			405						410					415	
Ala	Ala	Leu	Lys	Glu	Lys	Leu	Ser	Glu	Asn						
			420					425							

References.

1. Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J. Mol. Biol. 3, 208-218.
2. Fleishmann, R.D. et al. (1995) Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd. Science 269, 496-512.
3. Borodovsky M, Rudd KE, and EV Koonin. (1994). Intrinsic and extrinsic approaches for detecting genes in a bacterial genome. Nucleic Acids Res. 22:4756-4767.
4. Horton, P. and Nakai, K. (1996). A probabilistic classification system for predicting the cellular localization sites of proteins. Intellig. Syst. Mol. Biol. 4: 109-115.
5. Claros MG and G von Heijne. (1994). TopPred II: an improved software for membrane protein structure predictions. Comput. Appl. Biosci. 10: 685-686.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this 5th day of May 1998

CSL LIMITED

Patent Attorneys for the Applicant:

F.B. RICE & CO.

